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ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTICTGATACCGAAACCACCGGTATGAACCAGATTGGT 75
-----mutD-----
M T A M S T A I T R Q I V L D T E T T G M N Q I G
GCGCACTATGAAGGCCACAAGATCATTGAGATTGGTCCGTGAAGTGGTGAACCGTCGCCCTGACGGGCAATAAC 150
-----mutD-----
A H Y E G H K I I E I G A V E V N R R L T G N N
TTCCATGTTTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTGGCGTACATGGTATGCCGATGAATTT 225
-----mutD-----
F H V Y L K P D R L V D P E A F G V H G I A D E F
TTGCTCGATAAGCCCACGTTTGCCGAAGTAGCCGATGAGTTCAATGGACTATATTCGCGCGGAGTTGGTGATC 300
-----mutD-----
L L D K P T F A E V A D E F M D Y I R G A E L V I
CATAACGAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGCGATATCCGAAGACCAAT 375
-----mutD-----
H N A A F D I G F M D Y E F S L L K R D I P K T N

FIG..1A

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ACTTTCGTAAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAATGTTTCCCGGTAAAGCGCAACAGCCTCGATGCG 450

mutD

T F C K V T D S L A V A R K M F P G K R N S L D A

TTATGTGCTCGCTACGAAATAGATAACAGTAAACGACGCTGCACGGGGCATTACTCGATGCCCGAGATCCTTGCG 525

mutD

L C A R Y E I D N S K R T L H G A L L D A Q I L A

GAAGTTTATCTGGCGATGACCGGTGGTCAACGCTCGATGGCTTTTGGCATGGAAGGAGAGACACACAGCAACAA 600

mutD

E V Y L A M T G G Q T S M A F A M E G E T Q Q Q Q

GGTGAAGCAACAATTCAGCGCATTGTACGTCAGGCAAGTAAGTTACGCGTTGTTTTGCGACAGATGAAGAGATT 675

mutD

G E A T I O R I V R Q A S K L R V V F A T D E E I

GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAAGAAAGCGGAAGTTGCCTCTGGCGAGCATAA 741

mutD

A A H E A R L D L V Q K K G G S C L W R A .

FIG. 1B

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10  ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTGAACCTTCTTTGGCCCGGGCGCC Eb_429T.dna
10  ATGAGCTATCGTATGTTTGAATTAATCTGGTTCCAAATGTGAACCTTCTTTGGCCCGGGCGCC Eb_GEBT.dna

70  GTTTCCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAATAAGCCCTGCTGGTGACCC Eb_429T.dna
70  GTTTCCTGTTGTTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAATAAGCCCTGCTGGTGACCC Eb_GEBT.dna

130 GATAAGGGCCCTGCCGCGCCATTAAAGACGGTGCTGTCGATCAGACCCGTGAAGCACCTGAAA Eb_429T.dna
130 GATAAGGGCCCTGCCGCGCCATTAAAGACGGTGCTGTCGATCAGACCCGTGAAGCACCTGAAA Eb_GEBT.dna

190 GCCGCCGGTATTGAGGTGGTCAATTTTCGACGGGGTTCGAGCCGAAACCCGAAAGACACCAAC Eb_429T.dna
190 GCCGCCGGTATTGAGGTGGTCAATTTTCGACGGGGTTCGAGCCGAAACCCGAAAGACACCAAC Eb_GEBT.dna

250 GTGCTCGACGGCCCTGGCCCATGTTCCGTAAGAGCAGTGGCGACATGATAATCACCGTCGGC Eb_429T.dna
250 GTGCTCGACGGCCCTGGCCCATGTTCCGTAAGAGCAGTGGCGACATGATAATCACCGTCGGC Eb_GEBT.dna
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FIG.--2A

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310  GCGGGCAGCCCGCAACGACTGCGGGTAAGGCA TTGGTATTGCGGGCCACCCACCGGGTGAT Eb_429T.dna
310  GCGGGCAGCCCGCTCGACTGCGGGTAAGGCA TTGGTATTGCGGGCCACCCACCGGGTGAT Eb_GEBT.dna

370  CTGTACAGCTATGCCGGGTATCGAAACA CTCAACCAACCCGGCTGCCGCCCATTTATTGCGGGTTC Eb_429T.dna
370  CTGTACAGCTATGCCGGGTATCGAAACA CTCAACCAACCCGGCTGCCGCCCATTTATTGCGGGTTC Eb_GEBT.dna

430  AACACCAACCGCCGGGACCGCCAGCGGAAGTCA CCGGCCACTGCGTGCTGACTAACACCAAA Eb_429T.dna
430  AACACCAACCGCCGGGACCGCCAGCGGAAGTCA CCGGCCACTGCGTGCTGACTAACACCAAA Eb_GEBT.dna

490  ACCAAAGTAAATA TTGTGATTGTCA GCTGGCGGCAACCTGCGCTTCCGTTCTCCATTAAACGAT Eb_429T.dna
490  ACCAAAGTAAATA TTGTGATTGTCA GCTGGCGGCAACCTGCGCTTCCGTTCTCCATTAAACGAT Eb_GEBT.dna

550  CCGCTGCTGATGATCGGGCAAGCCCGCGGCTGACCGCCGCCACCGGGTATGGATGCCCTG Eb_429T.dna
550  CCGCTGCTGATGATCGGGCAAGCCCGCGGCTGACCGCCGCCACCGGGTATGGATGCCCTG Eb_GEBT.dna
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FIG._2B

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610	ACCCACGGGTAGAGGCCCTATATCTCCAAAGACGCCCAACCCGGTTACCGATGCCCTCTGCT	660	Eb_429T.dna
610	ACCCACGGGTAGAGGCCCTATATCTCCAAAGACGCCCAACCCGGTTACCGATGCCCTCTGCT		Eb_GEBT.dna
670	ATTACGGCCATCAAACTGATTGCCACCCAACTTGCGCCAGGCCCGTCGCCCTGGGGACCAAC	720	Eb_429T.dna
670	ATTACGGCCATCAAACTGATTGCCACCCAACTTGCGCCAGGCCCGTCGCCCTGGGGACCAAC		Eb_GEBT.dna
730	CTCAAAGCCCCGTGAAACAATGGCCCTGCGCCCTCTCTGCTGGCCCGGGATGGCCCTTTAACAAC	780	Eb_429T.dna
730	CTCAAAGCCCCGTGAAACAATGGCCCTGCGCCCTCTCTGCTGGCCCGGGATGGCCCTTTAACAAC		Eb_GEBT.dna
790	GCCAAACCTGGGCTATGTTCAAGCCCATGGCTCAACAGCTGGGCGGCCCTGTACGACATGGCC	840	Eb_429T.dna
790	GCCAAACCTGGGCTATGTTCAAGCCCATGGCTCAACAGCTGGGCGGCCCTGTACGACATGGCC		Eb_GEBT.dna
850	CACGGGGTGGCGGAACGCGGTCCTGCTGCCCCCATGTCTGCGCGCTATAACCTGATTGCCCAAC	900	Eb_429T.dna
850	CACGGGGTGGCGGAACGCGGTCCTGCTGCCCCCATGTCTGCGCGCTATAACCTGATTGCCCAAC		Eb_GEBT.dna

FIG..2C

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910	CCGGAAAAATTTGCCGATATCGCCACCTTTTATGGGGGAAACAACACCGGTCTTTCCACC	960	Eb_429T.dna
910	CCGGAAAAATTTGCCGATATCGCCACCTTTTATGGGGGAAACAACACCGGTCTTTCCACC		Eb_GEBT.dna
970	ATGGACGACGCGGAGCTGGCCCATCAGCGCCATTGGCCCGTCTGTCTAAAGATGTCGGGATC	1020	Eb_429T.dna
970	ATGGACGACGCGGAGCTGGCCCATCAGCGCCATTGGCCCGTCTGTCTAAAGATGTCGGGATC		Eb_GEBT.dna
1030	CCGCAGCACCTGCGGTGAACCTGGGGGTAAGAGAGGCCGACTTCCCGTACATGGCAGAAATG	1080	Eb_429T.dna
1030	CCGCAGCACCTGCGGTGAACCTGGGGGTAAGAGAGGCCGACTTCCCGTACATGGCAGAAATG		Eb_GEBT.dna
1090	GCCCTGAAGACGGCAACGGCCTTCTCTAACCCCGCGCAAGGGAAACGAAAGAGATTGCC	1140	Eb_429T.dna
1090	GCCCTGAAGACGGCAACGGCCTTCTCTAACCCCGCGCAAGGGAAACGAAAGAGATTGCC		Eb_GEBT.dna
1150	GACATTTTCCGCCAAGGCAATTCCTGA	1170	Eb_429T.dna
1150	GACATTTTCCGCCAAGGCAATTCCTGA		Eb_GEBT.dna

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG..2D

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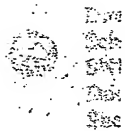
	10	40	70	100		
10	MSYRMFDYLV	PNVNF	FGPGAVSV	VGQRCQL	LGKKALLVT Eb_429T.dna	
10	MSYRMFDYLV	PNVNF	FGPGAVSV	VGQRCQL	LGKKALLVT Eb_GEBT.dna	
	130	160	190	220		
130	DKGLRAIKD	GAVDQT	VKHLKAAGI	EVVIFD	GVBP	NPKDTN Eb_429T.dna
130	DKGLRAIKD	GAVDQT	VKHLKAAGI	EVVIFD	GVBP	NPKDTN Eb_GEBT.dna
	250	280	310	340		
250	VLDGLAMFR	KEQC	DMIIIT	VGGGSP	HDCGKGIGIAATH	PGD Eb_429T.dna
250	VLDGLAMFR	KEQC	DMIIIT	VGGGSP	LDCGKGIGIAATH	PGD Eb_GEBT.dna
	370	400	430	460		
370	LYSYAGIET	LTNPLP	PIIAVNT	TAGTASE	VTRHCVLTNT	K Eb_429T.dna
370	LYSYAGIET	LTNPLP	PIIAVNT	TAGTASE	VTRHCVLTNT	K Eb_GEBT.dna
	490	520	550	580		
490	TKVKFPVIV	SWRNLP	SVSIND	PPLLMIGK	PAGLTAATGMDA	L Eb_429T.dna
490	TKVKFPVIV	SWRNLP	SVSIND	PPLLMIGK	PAGLTAATGMDA	L Eb_GEBT.dna

FIG._3A

610	THAVEAYISKDANPVT	640	670	700	Eb_429T.dna
610	THAVEAYISKDANPVT	640	670	700	Eb_GEBT.dna
730	LKARENMACASLLAGMAFN	760	790	820	Eb_429T.dna
730	LKARENMACASLLAGMAFN	760	790	820	Eb_GEBT.dna
850	HGVANAVLLPHVCRYNLI	880	910	940	Eb_429T.dna
850	HGVANAVLLPHVCRYNLI	880	910	940	Eb_GEBT.dna
970	MDAAELAISAIARLSKDV	1000	1030	1060	Eb_429T.dna
970	MDAAELAISAIARLSKDV	1000	1030	1060	Eb_GEBT.dna
1090	ALKDGNAPSNPRKGNBKE	1120	1150		Eb_429T.dna
1090	ALKDGNAPSNPRKGNBKE	1120	1150		Eb_GEBT.dna

Decoration "Decoration #1": Shade (with solid black) residues that differ from the Consensus.

FIG.-3B



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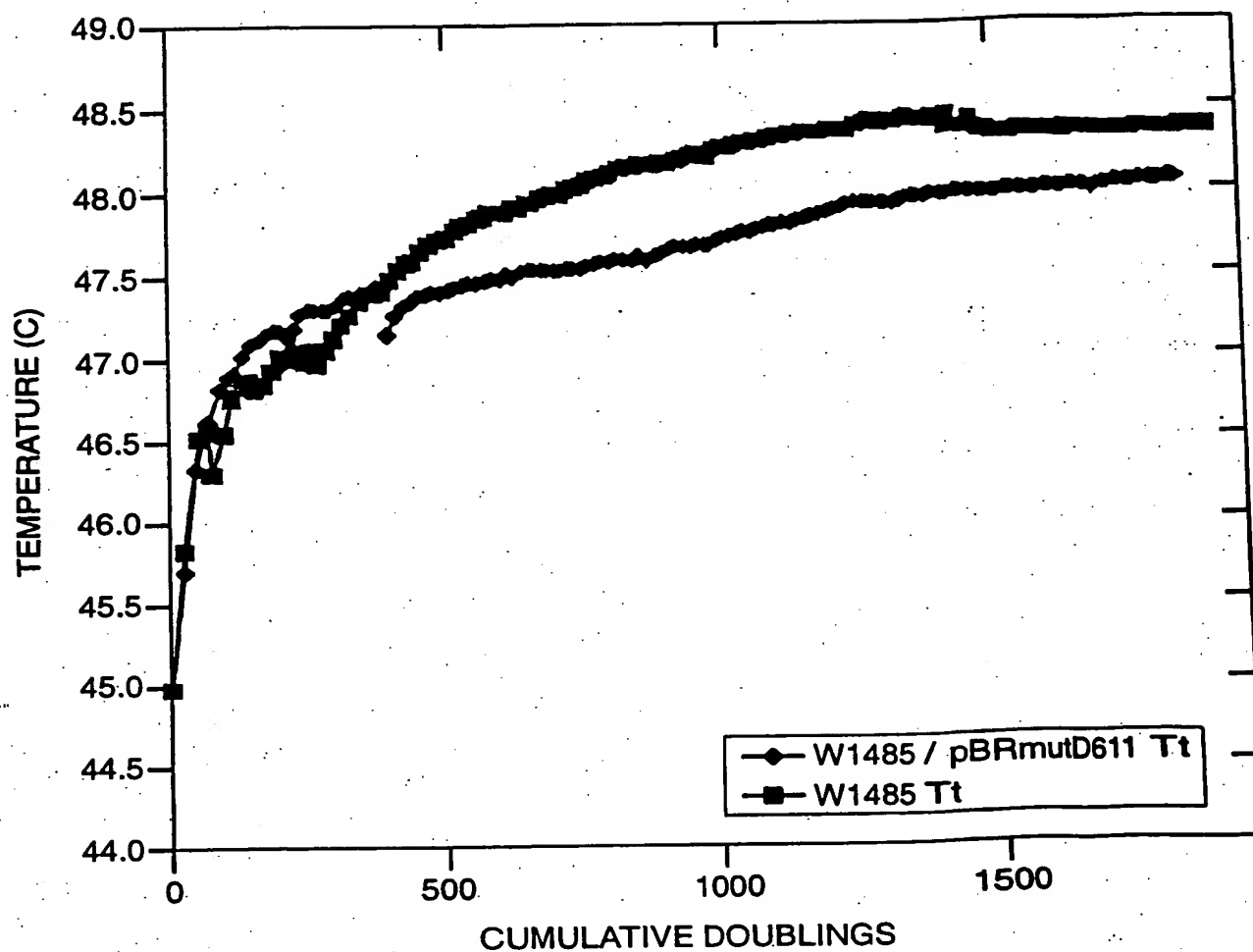


FIG. 4

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